

*Approved*  
*1/14/03***6943277**

GNCAGCATTTCCTCTAAGGGATNCAATNNGGCTTGCCCGAGGCCACACTCATTTCCTCCCATNCCC  
TCAAATACTGTGGTGATTAAACATTTTCATAGGAGGANTTTATGGATNCCTTTAAAANCCTAATT  
CTCCCTGCTTGCCAAATCATTTCCTCAGCATCCTGCCAGCAAAAAANCANCTTNTGATCAA  
AATNATCCCCGGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGNAGTCCNGGAGATTGCTGAC  
CGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATATGAAATATTCAAAGCCGTTGAGT  
ATAAACTCAAGTTGTCGCTGGAGTCAATTACTTTCATTAAGATGGATGTAGGGGGTGGTTGTTT  
CACCCACATAAAAGTCTTCAAGGATCTTTCTGGAAAGAATAATTTGGAACCTTACTGGTTACCAG  
ACTAACAAAACCGAGGATGATGAGCTGACCTACTTCTAAGCAGCAAATTCTAAAGTGACCTGAT  
TCCTCTCATTGTAACTGATTGNCATCAATAAAGAATATTCTCCA (SEQ ID NO:1)

**FIGURE 1**

09/104180



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TECH CENTER 1600/2900

underlined = deleted in targeting construct

[ ] = sequence flanking Neo insert in targeting construct

[GNCAGCATTTCTCTAAGGGATNCAATNMGGCTTGCCCGAGGCCCACTCATTTCCTCCCA  
 TNCCTCAAATACTGTGGTGATTAAACATTTTCATAGGAGGANTTTATGGATNCCTTTAAA  
 ANCCTAATTCTCCCTGCTTGCCAAATCATTCTTCTCAGCATCCTGCCAGCAAAAAANC  
 ANCTTNTGATCAAAATNATCCCCGAGGCTTNACGGAGGCCAGACCTGCCACAGCAGN]A  
GTCNNGGAGATTGCTGACCGGGTCAAAGCACAGCTCGANGAGGAAACCAATGAGAAATAT  
GAAATATTCAAAGCCGTTGAGTATAAACTCAAGTTGTCGCTGGAGTCAATTACTTCATT  
AAGATGGATGTAGGGGGTGGTGTGTTTCACCCACATAAAAAGTCTTCAAGGATCTTTCTGGA  
AAGAATAATTTGGAACCTTACTGGTTACCAGACTAACAAAACCGAGGATGATGAGCTGAC  
 CTACTTCTAAGCAGCAAAATTCTAAAGTGACCTGATTCTCTCATTGTAAACTGATTCGNC  
 CATCAATAAAGAATATTCTCCA]

Sub #8

FIGURE 2A

Approved  
PB  
1/14/07

OCT 28 2002

JCOB  
DEMARK OFFICE**Gene Sequence  
Structure\***

238 bp

Sequence Deleted

436 bp

Size of EST: 559 bp

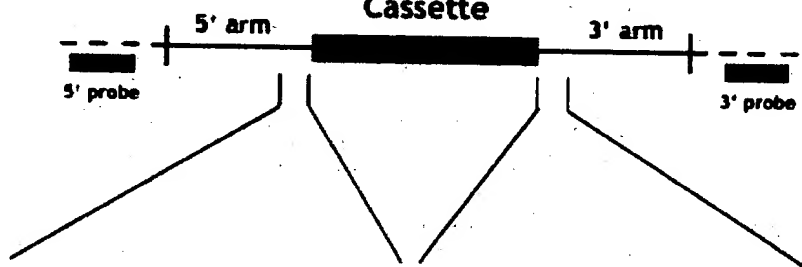
**Targeting Vector\*  
(genomic sequence)**

Construct Number: 2757

Arm Length:

5': 1.2 kb

3': 3 kb

**LacZ-Neo  
Cassette**

———— Targeting Vector  
 - - - - Endogenous Locus

\* Not drawn to scale

5' >CGAGGCCACACTCATTTC  
 ATTCCCTCAGATACTGTGATGATT  
 ATACATTTGATAGGAGGAGATTAT  
 GGATACCTTTAAAATTCTAAGTCT  
 CCCTGCTTGCCAGATCATTCTTC  
 TCAGCATTCTGCCCAGCAAAGAAG  
 CAACTCGTGATCAGAATGATACCC  
 GGAGGCTTGATGGAGGCCAGACCT  
 GCCACAGCAGA<3'  
 (SEQ ID NO:2)

5' >ACTGGTTACCAGACTAACAAA  
 ACCGAAGATGATGAAGTACCTAC  
 TTCTAAGCAGCAAATTCATAAGTC  
 ACCTGATTCCCTCTCATTGTAAACT  
 GATGCGGCCATCAATAAAGAAATA  
 TTCTTCAAATAAAAAAAAAAAGA  
 AAGAAGCATTCTAACACAATACAA  
 TCCAAAGATGTACTGATTTGATGT  
 TACATACTCAG<3'  
 (SEQ ID NO:3)

FIGURE 2B